

REMARKS

Claims 93, 119, 127-187 have been canceled without prejudice or disclaimer. Claims 77-81, 84-88, 90-92, 97, 113-126, 192-213 are pending. Claims 77-81, 84-88, 90-92, 121-125 and 192 are allowed. Claims 113, 118, 126, 193-208 and 213 have been amended, as follows. Claims 113 has been amended to delete position G433. Claims 118 and 126 have been amended to delete positions M15 and N188. Claims 193-208 and 213 have been amended to recite the transition term "consists of".

It is respectfully submitted that the present amendment presents no new issues or new matter and places this case in condition for allowance. Reconsideration of the application in view of the above amendments and the following remarks is requested.

I. The Rejection of Claims 93, 113, 118, 119, 126-128, 133, 134, 141, 158, 163-165, 171, 172, 186, 193, 200 and 207 under 35 U.S.C. 112

Claims 93, 113, 118, 119, 126-128, 133, 134, 141, 158, 163-165, 171, 172, 186, 193, 200 and 207 are rejected under 35 U.S.C. 112, as allegedly containing subject matter which was not described in the specification at the time the application was filed. The Examiner contends that the specification does not provide adequate support for claims that encompass mutations in positions corresponding to *Bacillus licheniformis* alpha amylase (SEQ ID NO:2) residues G433, M15, N188, M197 and/or K436.

Applicants have deleted positions G433, M15, and N188 from pending claims or have canceled claims comprising these positions in order to expedite prosecution. Accordingly, Applicants respectfully submit that the rejection of the claims based on positions G433, M15 and N188 is rendered moot by this Amendment.

With respect to position K436, Applicant respectfully submit that this position was not at issue in the claims examined by the Examiner, and therefore, Applicants respectfully request withdrawal of this rejection.

With respect to position M197, Applicants respectfully traverse the rejection. Variants comprising a mutation in a position corresponding to *Bacillus licheniformis* alpha amylase (SEQ ID NO:2) residue M197 is clearly found in the specification, including, among other places, at page 24, line 13.

For the foregoing reasons, Applicants submit that the claims overcome this rejection under 35 U.S.C. 112. Applicants respectfully request reconsideration and withdrawal of the rejection.

II. The Rejection of Claims 193-213 under 35 U.S.C. 112

Claims 193-213 are rejected under 35 U.S.C. 112 as allegedly non-enabled for the reasons set forth in the Office Action. The Examiner, however, states that amending the claims to recite "wherein the difference between said variant and said parent consists of a different amino acid residue" would obviate the rejection. Applicants have amended claims 193-213 in the manner suggested by the Examiner.

Therefore, Applicants submit that the claims overcome this rejection under 35 U.S.C. 112. Applicants respectfully request reconsideration and withdrawal of the rejection.

III. The Rejection of Claims 128-162, 166-170 and 173-187 under 35 U.S.C. 102(b)

Claims 128-162, 166-170 and 173-187 are rejected under 35 U.S.C. 102(b) as allegedly anticipated by Suzuki et al. Claims 128-162, 166-170, and 173-187 are canceled. Therefore Applicants respectfully request withdrawal of the rejection.

IV. Conclusion

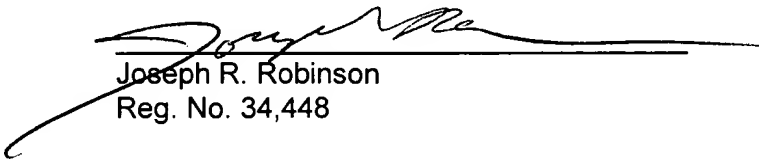
In view of the above, it is respectfully submitted that all claims are in condition for allowance. Early action to that end is respectfully requested. The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

Date: June 19, 2001

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Svendsen et al.

Serial No.: 09/327,563

Confirmation No:

Group Art Unit: 1652

Filed: June 8, 1999

Examiner: Slobodyansky

Confirmation No:

For: Alpha-Amylase Mutants

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Sir:

Below is a marked-up version of the amendments made in the accompanying amendment.

IN THE CLAIMS:

77. (Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to Q298 in *Bacillus licheniformis*.

78.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said

alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G299 in *Bacillus licheniformis*.

79.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G301 in *Bacillus licheniformis*.

80. (Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to Y302 in *Bacillus licheniformis*.

81.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to L307 in *Bacillus licheniformis*.

84.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to F343 in *Bacillus licheniformis*.

85.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to F403 in *Bacillus licheniformis*.

86.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to H405 in *Bacillus licheniformis*.

87.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to H406 in *Bacillus licheniformis*.

88.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to D407 in *Bacillus licheniformis*.

90.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to L427 in *Bacillus licheniformis*.

91.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby

alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to I428 in *Bacillus licheniformis*.

92.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to D430 in *Bacillus licheniformis*.

97.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G475 in *Bacillus licheniformis*.

113. (Twice Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, [G433,] and G475 in *Bacillus licheniformis* (SEQ ID NO:2).

114.(Unchanged.) The alpha-amylase according to claim 113, wherein said alpha-amylase is produced by *Bacillus*.

115.(Unchanged.) The alpha-amylase according to claim 114, wherein said alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.

116.(Unchanged.) A detergent comprising the alpha-amylase according to claim 113.

117.(Unchanged.) A starch liquefaction composition comprising the alpha-amylase according to claim 113.

118. (Amended.) The alpha-amylase according to claim 113, wherein said alpha- amylase further comprises a substitution or deletion at one or more residues equivalent to [M15, N188,] A209 and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

120. (Unchanged.) The alpha-amylase according to claim 113 which is modified by substituting an amino acid residue at a position corresponding to one or more of G301, H405 and/or H406 in *Bacillus licheniformis*.

121.(Unchanged.) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407,

I428, D430, and G475 in *Bacillus licheniformis* (SEQ ID NO:2).

122.(Unchanged.) The alpha-amylase according to claim 121, wherein said alpha-amylase is produced by *Bacillus*.

123.(Unchanged.) The alpha-amylase according to claim 122, wherein said alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.

124.(Unchanged.) A detergent comprising the alpha-amylase according to claim 121.

125.(Unchanged.) A starch liquefaction composition comprising the alpha-amylase according to claim 121.

126. (Amended.) The alpha-amylase according to claim 121, wherein said alpha-amylase further comprises a substitution or deletion at one or more residues equivalent to [M15, N188,] A209 and/or M197.

192.(Unchanged.) A variant of a parent alpha-amylase, said parent alpha-amylase having SEQ ID NO:2, in which variant the amino acid residues 325-345 of the parent alpha-amylase have been replaced with amino acid residues 294-313 of SEQ ID No.10.

193.(Amended.) A variant of a parent alpha-amylase, said variant having an amino acid sequence which differs from the amino acid sequence of said parent, wherein the difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at one or more positions selected from the group consisting of

the positions which correspond to amino acid residues Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2); wherein said variant has alpha-amylase activity.

194.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue Q298 in *Bacillus licheniformis* alpha-amylase. --

195.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G299 in *Bacillus licheniformis* alpha-amylase. --

196.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G301 in *Bacillus licheniformis* alpha-amylase. --

197.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue Y302 in *Bacillus licheniformis* alpha-amylase. --

198.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue L307 in *Bacillus licheniformis* alpha-amylase. --

199.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue F343 in *Bacillus*

licheniformis alpha-amylase. --

200.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue F403 in *Bacillus licheniformis* alpha-amylase. --

201.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue H405 in *Bacillus licheniformis* alpha-amylase. --

202.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue H406 in *Bacillus licheniformis* alpha-amylase. --

203.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue D407 in *Bacillus licheniformis* alpha-amylase. --

204.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G427 in *Bacillus licheniformis* alpha-amylase. --

205.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue I428 in *Bacillus licheniformis* alpha-amylase. --

206.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue D430 in *Bacillus licheniformis* alpha-amylase.

207.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G433 in *Bacillus licheniformis* alpha-amylase. --

208.(Amended.) The variant according to claim 193, wherein said difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at the position which corresponds to amino acid residue G475 in *Bacillus licheniformis* alpha-amylase. --

209.(Unchanged.) The variant according to claim 193, wherein said parent alpha-amylase is produced by *Bacillus*.--

210.(Unchanged.) The variant according to claim 193, wherein said parent alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.--

211.(Unchanged.) A detergent comprising the variant according to claim 193.--

212.(Unchanged.) A starch liquefaction composition comprising the variant according to claim 193.--

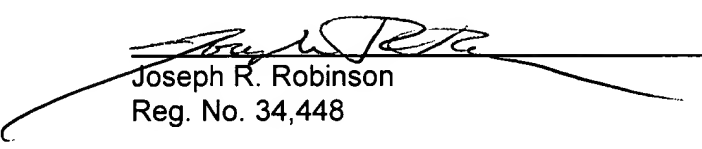
213.(Amended.) A variant of a parent alpha-amylase, said variant having an amino acid sequence which differs from the amino acid sequence of said parent, wherein the difference between said variant and said parent [comprises] consists of a different amino acid residue in said variant than in said parent at one or more positions selected from the group consisting of the positions which correspond to amino acid residues Q298, G299, G301, Y302, L307, H405,

H406, D407, I428, D430, and G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2);
wherein said variant has alpha-amylase activity.

Respectfully submitted,

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